



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/799,782

DATE: 09/01/2004
TIME: 13:01:12

Input Set : N:\CrF3\RULE60\10799782.raw
Output Set: N:\CRF4\09012004\J799782.raw

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:

2 (i) APPLICANT: Ullrich, Axel
3 Risau, Werner
4 Millauer, Birgit
5 Gazit, Aviv
6 Levitzki, Alex

7 (ii) TITLE OF INVENTION: Flk-1 Is A Receptor For Vascular
8 Endothelial Growth Factor

9 (iii) NUMBER OF SEQUENCES: 6

10 (iv) CORRESPONDENCE ADDRESS:
11 (A) ADDRESSEE: Pennie & Edmonds
12 (B) STREET: 1155 Avenue of the Americas
13 (C) CITY: New York
14 (D) STATE: New York
15 (E) COUNTRY: U.S.A.
16 (F) ZIP: 10036-2711

17 (v) COMPUTER READABLE FORM:
18 (A) MEDIUM TYPE: Floppy disk
19 (B) COMPUTER: IBM PC compatible
20 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
21 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

22 (vi) CURRENT APPLICATION DATA:
23 (A) APPLICATION NUMBER: US/10/799,782
24 (B) FILING DATE: 15-Mar-2004
25 (C) CLASSIFICATION:

26 (vii) PRIOR APPLICATION DATA:
27 (A) APPLICATION NUMBER: US/09/766,678
28 (B) FILING DATE: 25-Jan-2001
29 (A) APPLICATION NUMBER: 08/193,829
30 (B) FILING DATE: 09-FEB-1994

31 (viii) ATTORNEY/AGENT INFORMATION:
32 (A) NAME: Coruzzi, Laura A.
33 (B) REGISTRATION NUMBER: 30,742
34 (C) REFERENCE/DOCKET NUMBER: 7683-060

35 (ix) TELECOMMUNICATION INFORMATION:
36 (A) TELEPHONE: (212) 790-9090
37 (B) TELEFAX: (212) 869-9741
38 (C) TELEX: 66141 PENNIE

39 (2) INFORMATION FOR SEQ ID NO: 1:

40 (i) SEQUENCE CHARACTERISTICS:
41 (A) LENGTH: 5470 base pairs
42 (B) TYPE: nucleic acid

43

ENTERED

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44 (C) STRANDEDNESS: unknown
45 (D) TOPOLOGY: unknown
W--> 46 (i.i) MOLECULE TYPE: DNA
47 (ix) FEATURE:
48 (A) NAME/KEY: CDS
49 (B) LOCATION: 286..4386
50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
51 TATAGGGCGA ATTGGGTACG GGACCCCCCT CGAGGTCGAC GGTATCGATA AGCTTGATAT 60
52 CGAATTCTGGG CCCAGACTGT GTCCCGCAGC CGGGATAACC TGGCTGACCC GATTCCCGGG 120
53 ACACCGCTGA CAGCCGCGGC TGGAGCCAGG GCGCCGGTGC CCCGCGCTCT CCCC GGTC 180
54 GCGCTGCGGG GCCATACCG CCTCTGTGAC TTCTTGCGG GCCAGGGACG GAGAAGGAGT 240
55 CTGTGCCTGA GAAACTGGGC TCTGTGCCCA GGCGCGAGGT GCAGG ATG GAG AGC 294
56 Met Glu Ser
57 1
58 AAG GCG CTG CTA GCT GTC GCT CTG TGG TTC TGC GTG GAG ACC CGA GCC 342
59 Lys Ala Leu Leu Ala Val Ala Leu Trp Phe Cys Val Glu Thr Arg Ala
60 5 10 15
61 GCC TCT GTG GGT TTG ACT GGC GAT TTT CTC CAT CCC CCC AAG CTC AGC 390
62 Ala Ser Val Gly Leu Thr Gly Asp Phe Leu His Pro Pro Lys Leu Ser
63 20 25 30 35
64 ACA CAG AAA GAC ATA CTG ACA ATT TTG GCA AAT ACA ACC CTT CAG ATT 438
65 Thr Gln Lys Asp Ile Leu Thr Ile Leu Ala Asn Thr Thr Leu Gln Ile
66 40 45 50
67 ACT TGC AGG GGA CAG CGG GAC CTG GAC TGG CTT TGG CCC AAT GCT CAG 486
68 Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro Asn Ala Gln
69 55 60 65
70 CGT GAT TCT GAG GAA AGG GTA TTG GTG ACT GAA TGC GGC GGT GGT GAC 534
71 Arg Asp Ser Glu Glu Arg Val Leu Val Thr Glu Cys Gly Gly Asp
72 70 75 80
73 AGT ATC TTC TGC AAA ACA CTC ACC ATT CCC AGG GTG GTT GGA AAT GAT 582
74 Ser Ile Phe Cys Lys Thr Leu Thr Ile Pro Arg Val Val Gly Asn Asp
75 85 90 95
76 ACT GGA GCC TAC AAG TGC TCG TAC CGG GAC GTC GAC ATA GCC TCC ACT 630
77 Thr Gly Ala Tyr Lys Cys Ser Tyr Arg Asp Val Asp Ile Ala Ser Thr
78 100 105 110 115
79 GTT TAT GTC TAT GTT CGA GAT TAC AGA TCA CCA TTC ATC GCC TCT GTC 678
80 Val Tyr Val Tyr Val Arg Asp Tyr Arg Ser Pro Phe Ile Ala Ser Val
81 120 125 130
82 AGT GAC CAG CAT GGC ATC GTG TAC ATC ACC GAG AAC AAG AAC AAA ACT 726
83 Ser Asp Gln His Gly Ile Val Tyr Ile Thr Glu Asn Lys Asn Lys Thr
84 135 140 145
85 GTG GTG ATC CCC TGC CGA GGG TCG ATT TCA AAC CTC AAT GTG TCT CTT 774
86 Val Val Ile Pro Cys Arg Gly Ser Ile Ser Asn Leu Asn Val Ser Leu
87 150 155 160
88 TGC GCT AGG TAT CCA GAA AAG AGA TTT GTT CCG GAT GGA AAC AGA ATT 822
89 Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg Ile
90 165 170 175
91 TCC TGG GAC AGC GAG ATA GGC TTT ACT CTC CCC AGT TAC ATG ATC AGC 870
92 Ser Trp Asp Ser Glu Ile Gly Phe Thr Leu Pro Ser Tyr Met Ile Ser

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93	180	185	190	195													
94	TAT	GCC	GGC	ATG	GTC	TTC	TGT	GAG	GCA	AAG	ATC	AAT	GAT	GAA	ACC	TAT	918
95	Tyr	Ala	Gly	Met	Val	Phe	Cys	Glu	Ala	Lys	Ile	Asn	Asp	Glu	Thr	Tyr	
96				200				205						210			
97	CAG	TCT	ATC	ATG	TAC	ATA	GTT	GTG	GTT	GTA	GGA	TAT	AGG	ATT	TAT	GAT	966
98	Gln	Ser	Ile	Met	Tyr	Ile	Val	Val	Val	Val	Gly	Tyr	Arg	Ile	Tyr	Asp	
99				215				220						225			
100	GTG	ATT	CTG	AGC	CCC	CCG	CAT	GAA	ATT	GAG	CTA	TCT	GCC	GGA	GAA	AAA	1014
101	Val	Ile	Leu	Ser	Pro	Pro	His	Glu	Ile	Glu	Leu	Ser	Ala	Gly	Glu	Lys	
102				230				235						240			
103	CTT	GTC	TTA	AAT	TGT	ACA	GCG	AGA	ACA	GAG	CTC	AAT	GTG	GGG	CTT	GAT	1062
104	Leu	Val	Leu	Asn	Cys	Thr	Ala	Arg	Thr	Glu	Leu	Asn	Val	Gly	Leu	Asp	
105				245				250						255			
106	TTC	ACC	TGG	CAC	TCT	CCA	CCT	TCA	AAG	TCT	CAT	CAT	AAG	AAG	ATT	GTA	1110
107	Phe	Thr	Trp	His	Ser	Pro	Pro	Ser	Lys	Ser	His	His	Lys	Lys	Ile	Val	
108				260				265						270		275	
109	AAC	CGG	GAT	GTG	AAA	CCC	TTT	CCT	GGG	ACT	GTG	GCG	AAG	ATG	TTT	TTG	1158
110	Asn	Arg	Asp	Val	Lys	Pro	Phe	Pro	Gly	Thr	Val	Ala	Lys	Met	Phe	Leu	
111				280				285						290			
112	AGC	ACC	TTG	ACA	ATA	GAA	AGT	GTG	ACC	AAG	AGT	GAC	CAA	GGG	GAA	TAC	1206
113	Ser	Thr	Leu	Thr	Ile	Glu	Ser	Val	Thr	Lys	Ser	Asp	Gln	Gly	Glu	Tyr	
114				295				300						305			
115	ACC	TGT	GTA	GCG	TCC	AGT	GGA	CGG	ATG	ATC	AAG	AGA	AAT	AGA	ACA	TTT	1254
116	Thr	Cys	Val	Ala	Ser	Ser	Gly	Arg	Met	Ile	Lys	Arg	Asn	Arg	Thr	Phe	
117				310				315						320			
118	GTC	CGA	GTT	CAC	ACA	AAG	CCT	TTT	ATT	GCT	TTC	GGT	AGT	GGG	ATG	AAA	1302
119	Val	Arg	Val	His	Thr	Lys	Pro	Phe	Ile	Ala	Phe	Gly	Ser	Gly	Met	Lys	
120				325				330						335			
121	TCT	TTG	GTG	GAA	GCC	ACA	GTG	GGC	AGT	CAA	GTC	CGA	ATC	CCT	GTG	AAG	1350
122	Ser	Leu	Val	Glu	Ala	Thr	Val	Gly	Ser	Gln	Val	Arg	Ile	Pro	Val	Lys	
123				340				345						350		355	
124	TAT	CTC	AGT	TAC	CCA	GCT	CCT	GAT	ATC	AAA	TGG	TAC	AGA	AAT	GGA	AGG	1398
125	Tyr	Leu	Ser	Tyr	Pro	Ala	Pro	Asp	Ile	Lys	Trp	Tyr	Arg	Asn	Gly	Arg	
126				360				365						370			
127	CCC	ATT	GAG	TCC	AAC	TAC	ACA	ATG	ATT	GTT	GGC	GAT	GAA	CTC	ACC	ATC	1446
128	Pro	Ile	Glu	Ser	Asn	Tyr	Thr	Met	Ile	Val	Gly	Asp	Glu	Leu	Thr	Ile	
129				375				380						385			
130	ATG	GAA	GTG	ACT	GAA	AGA	GAT	GCA	GGA	AAC	TAC	ACG	GTC	ATC	CTC	ACC	1494
131	Met	Glu	Val	Thr	Glu	Arg	Asp	Ala	Gly	Asn	Tyr	Thr	Val	Ile	Leu	Thr	
132				390				395						400			
133	AAC	CCC	ATT	TCA	ATG	GAG	AAA	CAG	AGC	CAC	ATG	GTC	TCT	CTG	GTT	GTG	1542
134	Asn	Pro	Ile	Ser	Met	Glu	Lys	Gln	Ser	His	Met	Val	Ser	Leu	Val	Val	
135				405				410						415			
136	AAT	GTC	CCA	CCC	CAG	ATC	GGT	GAG	AAA	GCC	TTG	ATC	TCG	CCT	ATG	GAT	1590
137	Asn	Val	Pro	Pro	Gln	Ile	Gly	Glu	Lys	Ala	Leu	Ile	Ser	Pro	Met	Asp	
138				420				425						430		435	
139	TCC	TAC	CAG	TAT	GGG	ACC	ATG	CAG	ACA	TTG	ACA	TGC	ACA	GTC	TAC	GCC	1638
140	Ser	Tyr	Gln	Tyr	Gly	Thr	Met	Gln	Thr	Leu	Thr	Cys	Thr	Val	Tyr	Ala	
141				440				445						450			

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142 AAC CCT CCC CTG CAC CAC ATC CAG TGG TAC TGG CAG CTA GAA GAA GCC	1686
143 Asn Pro Pro Leu His His Ile Gln Trp Tyr Trp Gln Leu Glu Glu Ala	
144 455 460 465	
145 TGC TCC TAC AGA CCC GGC CAA ACA AGC CCG TAT GCT TGT AAA GAA TGG	1734
146 Cys Ser Tyr Arg Pro Gly Gln Thr Ser Pro Tyr Ala Cys Lys Glu Trp	
147 470 475 480	
148 AGA CAC GTG GAG GAT TTC CAG GGG GGA AAC AAG ATC GAA GTC ACC AAA	1782
149 Arg His Val Glu Asp Phe Gln Gly Gly Asn Lys Ile Glu Val Thr Lys	
150 485 490 495	
151 AAC CAA TAT GCC CTG ATT GAA GGA AAA AAC AAA ACT GTA AGT ACG CTG	1830
152 Asn Gln Tyr Ala Leu Ile Glu Gly Lys Asn Lys Thr Val Ser Thr Leu	
153 500 505 510 515	
154 GTC ATC CAA GCT GCC AAC GTG TCA GCG TTG TAC AAA TGT GAA GCC ATC	1878
155 Val Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr Lys Cys Glu Ala Ile	
156 520 525 530	
157 AAC AAA GCG GGA CGA GGA GAG AGG GTC ATC TCC TTC CAT GTG ATC AGG	1926
158 Asn Lys Ala Gly Arg Gly Glu Arg Val Ile Ser Phe His Val Ile Arg	
159 535 540 545	
160 GGT CCT GAA ATT ACT GTG CAA CCT GCT GCC CAG CCA ACT GAG CAG GAG	1974
161 Gly Pro Glu Ile Thr Val Gln Pro Ala Ala Gln Pro Thr Glu Gln Glu	
162 550 555 560	
163 AGT GTG TCC CTG TTG TGC ACT GCA GAC AGA AAT ACG TTT GAG AAC CTC	2022
164 Ser Val Ser Leu Leu Cys Thr Ala Asp Arg Asn Thr Phe Glu Asn Leu	
165 565 570 575	
166 ACG TGG TAC AAG CTT GGC TCA CAG GCA ACA TCG GTC CAC ATG GGC GAA	2070
167 Thr Trp Tyr Lys Leu Gly Ser Gln Ala Thr Ser Val His Met Gly Glu	
168 580 585 590 595	
169 TCA CTC ACA CCA GTT TGC AAG AAC TTG GAT GCT CTT TGG AAA CTG AAT	2118
170 Ser Leu Thr Pro Val Cys Lys Asn Leu Asp Ala Leu Trp Lys Leu Asn	
171 600 605 610	
172 GGC ACC ATG TTT TCT AAC AGC ACA AAT GAC ATC TTG ATT GTG GCA TTT	2166
173 Gly Thr Met Phe Ser Asn Ser Thr Asn Asp Ile Leu Ile Val Ala Phe	
174 615 620 625	
175 CAG AAT GCC TCT CTG CAG GAC CAA GGC GAC TAT GTT TGC TCT GCT CAA	2214
176 Gln Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr Val Cys Ser Ala Gln	
177 630 635 640	
178 GAT AAG AAG ACC AAG AAA AGA CAT TGC CTG GTC AAA CAG CTC ATC ATC	2262
179 Asp Lys Lys Thr Lys Lys Arg His Cys Leu Val Lys Gln Leu Ile Ile	
180 645 650 655	
181 CTA GAG CGC ATG GCA CCC ATG ATC ACC GGA AAT CTG GAG AAT CAG ACA	2310
182 Leu Glu Arg Met Ala Pro Met Ile Thr Gly Asn Leu Glu Asn Gln Thr	
183 660 665 670 675	
184 ACA ACC ATT GGC GAG ACC ATT GAA GTG ACT TGC CCA GCA TCT GGA AAT	2358
185 Thr Thr Ile Gly Glu Thr Ile Glu Val Thr Cys Pro Ala Ser Gly Asn	
186 680 685 690	
187 CCT ACC CCA CAC ATT ACA TGG TTC AAA GAC AAC GAG ACC CTG GTA GAA	2406
188 Pro Thr Pro His Ile Thr Trp Phe Lys Asp Asn Glu Thr Leu Val Glu	
189 695 700 705	
190 GAT TCA GGC ATT GTA CTG AGA GAT GGG AAC CGG AAC CTG ACT ATC CGC	2454

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191	Asp	Ser	Gly	Ile	Val	Leu	Arg	Asp	Gly	Asn	Arg	Asn	Leu	Thr	Ile	Arg	
192				710				715					720				
193	AGG	GTG	AGG	AAG	GAG	GAT	GGG	GGC	CTC	TAC	ACC	TGC	CAG	GCC	TGC	AAT	2502
194	Arg	Val	Arg	Lys	Glu	Asp	Gly	Gly	Leu	Tyr	Thr	Cys	Gln	Ala	Cys	Asn	
195				725				730				735					
196	GTC	CTT	GGC	TGT	GCA	AGA	GCG	GAG	ACG	CTC	TTC	ATA	ATA	GAA	GGT	GCC	
197	Val	Leu	Gly	Cys	Ala	Arg	Ala	Glu	Thr	Leu	Phe	Ile	Ile	Glu	Gly	Ala	2550
198	740				745				750			755					
199	CAG	GAA	AAG	ACC	AAC	TTG	GAA	GTC	ATT	ATC	CTC	GTC	GGC	ACT	GCA	GTG	
200	Gln	Glu	Lys	Thr	Asn	Leu	Glu	Val	Ile	Ile	Leu	Val	Gly	Thr	Ala	Val	
201				760				765			770						
202	ATT	GCC	ATG	TTC	TTC	TGG	CTC	CTT	CTT	GTC	ATT	GTC	CTA	CGG	ACC	GTT	2646
203	Ile	Ala	Met	Phe	Phe	Trp	Leu	Leu	Leu	Val	Ile	Val	Leu	Arg	Thr	Val	
204				775				780			785						
205	AAG	CGG	GCC	AAT	GAA	GGG	GAA	CTG	AAG	ACA	GGC	TAC	TTG	TCT	ATT	GTC	2694
206	Lys	Arg	Ala	Asn	Glu	Gly	Glu	Leu	Lys	Thr	Gly	Tyr	Leu	Ser	Ile	Val	
207				790				795			800						
208	ATG	GAT	CCA	GAT	GAA	TTG	CCC	TTG	GAT	GAG	CGC	TGT	GAA	CGC	TTG	CCT	2742
209	Met	Asp	Pro	Asp	Glu	Leu	Pro	Leu	Asp	Glu	Arg	Cys	Glu	Arg	Leu	Pro	
210				805				810			815						
211	TAT	GAT	GCC	AGC	AAG	TGG	GAA	TTC	CCC	AGG	GAC	CGG	CTG	AAA	CTA	GGA	2790
212	Tyr	Asp	Ala	Ser	Lys	Trp	Glu	Phe	Pro	Arg	Asp	Arg	Leu	Lys	Leu	Gly	
213	820				825				830			835					
214	AAA	CCT	CTT	GGC	CGC	GGT	GCC	TTC	GGC	CAA	GTG	ATT	GAG	GCA	GAC	GCT	2838
215	Lys	Pro	Leu	Gly	Arg	Gly	Ala	Phe	Gly	Gln	Val	Ile	Glu	Ala	Asp	Ala	
216				840				845			850						
217	TTT	GGA	ATT	GAC	AAG	ACA	GCG	ACT	TGC	AAA	ACA	GTA	GCC	GTC	AAG	ATG	2886
218	Phe	Gly	Ile	Asp	Lys	Thr	Ala	Thr	Cys	Lys	Thr	Val	Ala	Val	Lys	Met	
219				855				860			865						
220	TTG	AAA	GAA	GGA	GCA	ACA	CAC	AGC	GAG	CAT	CGA	GCC	CTC	ATG	TCT	GAA	2934
221	Leu	Lys	Glu	Gly	Ala	Thr	His	Ser	Glu	His	Arg	Ala	Leu	Met	Ser	Glu	
222				870				875			880						
223	CTC	AAG	ATC	CTC	ATC	CAC	ATT	GGT	CAC	CAT	CTC	AAT	GTG	GTG	AAC	CTC	2982
224	Leu	Lys	Ile	Leu	Ile	His	Ile	Gly	His	His	His	Leu	Asn	Val	Val	Asn	
225				885				890			895						
226	CTA	GGC	GCC	TGC	ACC	AAG	CCG	GGA	GGG	CCT	CTC	ATG	GTG	ATT	GTG	GAA	3030
227	Leu	Gly	Ala	Cys	Thr	Lys	Pro	Gly	Gly	Pro	Leu	Met	Val	Ile	Val	Glu	
228	900				905				910			915					
229	TTC	TGC	AAG	TTT	GGA	AAC	CTA	TCA	ACT	TAC	TTA	CGG	GGC	AAG	AGA	AAT	3078
230	Phe	Cys	Lys	Phe	Gly	Asn	Leu	Ser	Thr	Tyr	Leu	Arg	Gly	Lys	Arg	Asn	
231				920				925			930						
232	GAA	TTT	GTT	CCC	TAT	AAG	AGC	AAA	GGG	GCA	CGC	TTC	CGC	CAG	GGC	AAG	3126
233	Glu	Phe	Val	Pro	Tyr	Lys	Ser	Lys	Gly	Ala	Arg	Phe	Arg	Gln	Gly	Lys	
234				935				940			945						
235	GAC	TAC	GTT	GGG	GAG	CTC	TCC	GTG	GAT	CTG	AAA	AGA	CGC	TTG	GAC	AGC	
236	Asp	Tyr	Val	Gly	Glu	Leu	Ser	Val	Asp	Leu	Lys	Arg	Arg	Leu	Asp	Ser	
237				950				955			960						
238	ATC	ACC	AGC	AGC	CAG	AGC	TCT	GCC	AGC	TCA	GGC	TTT	GTT	GAG	GAG	AAA	3222
239	Ile	Thr	Ser	Ser	Gln	Ser	Ser	Ala	Ser	Ser	Gly	Phe	Val	Glu	Glu	Lys	

VERIFICATION SUMMARY

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L:23 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:24 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:46 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1

L:521 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3

L:531 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4